SEQUENCE LISTING

<110> Stoddard, Barry L.
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<120> Crystal of a Truncated Protein Construct Containing a
      Coagulation Factor VIII C2 Domain in the Presence or
      Absence of a Bound Ligand and Methods of Use Thereof

<130> 14538A-005310US

<140> US 10/049,399
<141> Not yet assigned

<150> US 60/148,907
<151> 1999-08-13

<150> WO PCT/US00/22226
<151> 2000-08-11

<160> 12

<170> PatentIn Ver. 2.1

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<212> PRT
<213> Homo sapiens

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<223> human Factor VIII

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Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
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Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
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Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
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Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
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Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
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Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
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Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
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His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
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Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
            180             185             190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
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His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
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Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
225             230             235             240

Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His
            245             250             255

Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu
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Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile
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Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly
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Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met
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Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg
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Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp
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Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe
        355             360             365

Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His
    370             375             380

Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu
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Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro
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Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
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Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile
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2

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Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys
            485   490   495

His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys
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Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys
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Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala
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Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp
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Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe
            565   570   575

Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln
            580   585   590

Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe
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Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser
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Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr
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Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro
            660   665   670

Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp
        675   680   685

Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala
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Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu
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Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala
            725   730   735

Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Pro Ser Thr Arg
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Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys
        755   760   765

3

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Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser Pro Thr Pro
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His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr Glu Thr Phe
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Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn Ser Leu Ser
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Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val
        835             840             845

Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly
    850             855             860

Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser
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Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala
            885             890             895

Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met Pro Val His
        900             905             910

Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys Ser Ser Pro
        915             920             925

Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn Asn Asp
    930             935             940

Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp
945             950             955                 960

Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys
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Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys
        980             985             990

Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala
        995             1000            1005

Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser Leu Leu Ile Glu Asn
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Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser Asp Thr Glu Phe Lys
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Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp Lys Asn Ala
            1045            1050            1055

Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser Lys
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Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp
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Gly Gln Gly Pro Ser Pro Lys Gln Leu Val Ser Leu Gly Pro Glu Lys
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Ser Val Glu Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys Val Val Val
            1140             1145             1150

Gly Lys Gly Glu Phe Thr Lys Asp Val Gly Leu Lys Glu Met Val Phe
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Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp Asn Leu His Glu
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Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile Glu Lys
1185             1190             1195             1200

Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr
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Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr
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Arg Gln Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu
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Gln Asp Phe Arg Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His
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Thr Ala His Phe Ser Lys Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu
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Gly Asn Gln Thr Lys Gln Ile Val Glu Lys Tyr Ala Cys Thr Thr Arg
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Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe Val Thr Gln Arg Ser Lys
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Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu Thr Glu Leu Glu
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Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn Met
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Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys
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Glu Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg
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Ser His Ser Ile Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys
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Val Ser Ser Phe Pro Ser Ile Arg Pro Ile Tyr Leu Thr Arg Val Leu
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5

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Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr Gly Asp Gln
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Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr Tyr
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Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr
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Ser Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp
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Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu
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Val Glu Gly Ser Leu Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn
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Glu Ala Asn Arg Pro Gly Lys Val Pro Phe Leu Arg Val Ala Thr Glu
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Ser Ser Ala Lys Thr Pro Ser Lys Leu Leu Asp Pro Leu Ala Trp Asp
        1555            1560            1565

Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu Trp Lys Ser Gln Glu
    1570            1575            1580

Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile Leu Ser
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Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly
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Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr
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Glu Arg Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg
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Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr
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Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr
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Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg
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His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser
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Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg
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Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr
                1780            1785            1790

Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys
                1795            1800            1805

Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His Met Ala
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Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp
1825            1830            1835            1840

Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu
                1845            1850            1855

Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr
                1860            1865            1870

Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser
                1875            1880            1885

Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn
    1890            1895            1900

Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala
1905            1910            1915            1920

Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met Ala Gln
                1925            1930            1935

Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn
                1940            1945            1950

Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys Lys
                1955            1960            1965

Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu
    1970            1975            1980

Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys
1985            1990            1995          . 2000

Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val
                2005            2010            2015

Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile
                2020            2025            2030

Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro
    2035            2040            2045
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Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr
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Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile
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Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu
                2085                2090                2095

Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp
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Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly
                2115                2120                2125

Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile
    2130                2135                2140

Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser
2145                2150                2155                2160

Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met
                2165                2170                2175

Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala
                2180                2185                2190

Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala
                2195                2200                2205

Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn
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Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val
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Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr
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Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr
                2260                2265                2270

Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp
                2275                2280                2285

Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg
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Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg
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8

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human Factor
      VIII C2 domain

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      mutation)

<220>
<221> VARIANT
<222> (35)
<223> Xaa = Lys (wild-type) or Gln, Leu or Gly
      (hemophilia A mutations)

<220>
<221> VARIANT
<222> (54)
<223> Xaa = Pro (wild-type) or Cys (hemophilia A
      mutation)

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<223> Xaa = Met (wild-type) or Val (hemophilia A
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<220>
<221> VARIANT
<222> (73)
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       mutation)


<220>
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<220>
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<220>
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<222> (128)
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       mutation)


<220>
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<222> (132)
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Gln Ile Thr Xaa Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser
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Pro Ser Xaa Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg
            35                  40                  45

Pro Gln Val Asn Asn Xaa Lys Glu Trp Leu Gln Val Asp Phe Gln Lys
        50                  55                  60

Thr Xaa Lys Val Thr Gly Val Thr Xaa Xaa Gly Val Lys Ser Leu Leu
65                  70                  75                      80

Thr Ser Met Tyr Val Lys Glu Phe Leu Xaa Ser Ser Ser Gln Asp Gly
                85                  90                  95

His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Xaa Gln
                100                 105                 110

Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Xaa
            115                 120                 125

Leu Leu Thr Xaa Tyr Leu Xaa Ile His Pro Gln Ser Trp Val His Gln
    130                 135                 140

Ile Ala Leu Xaa Met Glu Val Leu Xaa Cys Glu Ala Gln Asp Leu Tyr
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<210> 8
<211> 160
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:murine Factor
      VIII C2 domain

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Ser Cys Ser Ile Pro Leu Gly Met Glu Ser Lys Val Ile Ser Asp Thr
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Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser
            20                  25                  30

Pro Ser Gln Ala Arg Leu His Leu Gln Gly Arg Thr Asn Ala Trp Arg
            35                  40                  45

Pro Gln Val Asn Asp Pro Lys Gln Trp Leu Gln Val Asp Leu Gln Lys
        50                  55                  60

Thr Met Lys Val Thr Gly Ile Ile Thr Gln Gly Val Lys Ser Leu Phe
65                  70                  75                      80

Thr Ser Met Phe Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly
                85                  90                  95
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His His Trp Thr Gln Ile Leu Tyr Asn Gly Lys Val Lys Val Phe Gln
            100   105   110

Gly Asn Gln Asp Ser Ser Thr Pro Met Met Asn Ser Leu Asp Pro Pro
            115   120   125

Leu Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ile Trp Glu His Gln
    130   135   140

Ile Ala Leu Arg Leu Glu Ile Leu Gly Cys Glu Ala Gln Gln Gln Tyr
145   150   155   160

<210> 9
<211> 160
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:canine Factor
      VIII C2 domain

<400> 9
Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala
  1   5   10   15

Gln Ile Thr Ala Ser Ser Tyr Leu Ser Ser Met Leu Ala Thr Trp Ser
            20   25   30

Pro Ser Gln Ala Arg Leu His Leu Gln Gly Arg Thr Asn Ala Trp Arg
            35   40   45

Pro Gln Ala Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Arg Lys
        50   55   60

Thr Met Lys Val Thr Gly Ile Thr Thr Gln Gly Val Lys Ser Leu Leu
 65   70   75   80

Ile Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly
                85   90   95

His Asn Trp Thr Leu Phe Leu Gln Asn Gly Lys Val Lys Val Phe Gln
            100   105   110

Gly Asn Arg Asp Ser Ser Thr Pro Val Arg Asn Arg Leu Glu Pro Pro
            115   120   125

Leu Val Ala Arg Tyr Val Arg Leu His Pro Gln Ser Trp Ala His His
    130   135   140

Ile Ala Leu Arg Leu Glu Val Leu Gly Cys Asp Thr Gln Gln Pro Ala
145   150   155   160

<210> 10
<211> 160
<212> PRT
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15

<220>
<223> Description of Artificial Sequence:porcine Factor
      VIII C2 domain

<400> 10
Ser Cys Ser Met Pro Leu Gly Met Gln Asn Lys Ala Ile Ser Asp Ser
1   5   10   15

Gln Ile Thr Ala Ser Ser His Leu Ser Asn Ile Phe Ala Thr Trp Ser
            20   25   30

Pro Ser Gln Ala Arg Leu His Leu Gln Gly Arg Thr Asn Ala Trp Arg
        35   40   45

Pro Arg Val Ser Ser Ala Glu Glu Trp Leu Gln Val Asp Leu Gln Lys
    50   55   60

Thr Val Lys Val Thr Gly Ile Thr Thr Gln Gly Val Lys Ser Leu Leu
65   70   75   80

Ser Ser Met Tyr Val Lys Glu Phe Leu Val Ser Ser Ser Gln Asp Gly
            85   90   95

Arg Arg Trp Thr Leu Phe Leu Gln Asp Gly His Thr Lys Val Phe Gln
            100   105   110

Gly Asn Gln Asp Ser Ser Thr Pro Val Val Asn Ala Leu Asp Pro Pro
        115   120   125

Leu Phe Thr Arg Tyr Leu Arg Ile His Pro Thr Ser Trp Ala Gln His
    130   135   140

Ile Ala Leu Arg Leu Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
145   150   155   160

<210> 11
<211> 159
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:porcine Factor
      V C2 domain

<400> 11
Gly Cys Ser Thr Pro Leu Gly Met Glu Asn Gly Lys Ile Glu Asn Lys
1   5   10   15

Gln Ile Thr Ala Ser Ser Phe Lys Lys Ser Trp Trp Gly Asp Tyr Trp
            20   25   30

Glu Pro Phe Arg Ala Arg Leu Asn Ala Gln Gly Arg Val Asn Ala Trp
        35   40   45

Gln Ala Lys Ala Asn Asn Asn Lys Gln Trp Leu Glu Ile Asp Leu Leu
    50   55   60

Lys Ile Lys Lys Ile Thr Ala Ile Ile Thr Gln Gly Cys Lys Ser Leu
65   70   75   80

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Ser Ser Glu Met Tyr Val Lys Ser Tyr Thr Ile His Tyr Ser Glu Gln
                85   90   95

Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser Ser Met Val Asp Lys
            100   105   110

Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His Val Lys Asn Phe Phe
        115   120   125

Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg Val Ile Pro Lys Thr Trp
    130   135   140

Asn Gln Ser Ile Ala Leu Arg Leu Glu Leu Phe Gly Cys Asp Ile
145   150   155

<210> 12
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human Factor
      VIII C1 domain

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Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala
            20   25   30

Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu Trp
            35   40   45

Ile Lys Val Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile Lys Thr
        50   55   60

Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile
65   70   75   80

Ile Met Tyr Ser Leu Asp Gly His His Trp Gln Thr Tyr Arg Gly Asn
            85   90   95

Ser Thr Gly Thr Leu Met Val Phe Gln Gly Asn Val Asp Ser Ser Gly
            100   105   110

Ile Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg
            115   120   125

Leu His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu
    130   135   140

Met Gly Cys Asp Leu Asn
145   150